



+T, O56C

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Malcolm, Bruce
Taremi, Shahriar S.
Weber, Patricia
Yao, Nanhua

(ii) TITLE OF INVENTION: Covalent Complexes of Hepatitis C Virus
NS3 Protease and NS4A Cofactor Peptide

(iii) NUMBER OF SEQUENCES: 123

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Schering-Plough Corp.
(B) STREET: 2000 Galloping Hill Road
(C) CITY: Kenilworth
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07030

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Power Macintosh
(C) OPERATING SYSTEM: 8.0.1
(D) SOFTWARE: Microsoft Word 6.0.1

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/198,723
(B) FILING DATE: 24 NOV 1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: McLaughlin, Jaye P.
(B) REGISTRATION NUMBER: 41,211
(C) REFERENCE/DOCKET NUMBER: JB0800

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (908)298-5056
(B) TELEFAX: (908)298-5388

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

S6

1	5	10	15												
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu
				20				25							30
Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu
				35				40							45
Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val
				50				55							60
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala
				65				70							80
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser
				85				90							95
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn
				100				105							110
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser
				115				120							125
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg
				130				135							140
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser
				145				150							160
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly
				165				170							175
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala
				180				185							190
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu
				195				200							205
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser								
				210				215							

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	
1				5				10						15	
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu

20

25

30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
 35 40 45

Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
 50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
 65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
 85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
 100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
 130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly
 165 170 175

Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
 180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
 195 200 205

Ser Met Glu Thr Thr Met Arg Ser
 210 215

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu

58

35	40	45
Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		
50	55	60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala		
65	70	75
80		
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser		
85	90	95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		
100	105	110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		
115	120	125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg		
130	135	140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser		
145	150	155
160		
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly		
165	170	175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala		
180	185	190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu		
195	200	205
Ser Met Glu Thr Thr Met Arg Ser		
210	215	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro		
1	5	10
15		
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu		
20	25	30
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu		
35	40	45
Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		

50	55	60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala		
65	70	75
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser		
85	90	95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		
100	105	110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		
115	120	125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg		
130	135	140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser		
145	150	155
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly		
165	170	175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala		
180	185	190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu		
195	200	205
Ser Met Glu Thr Thr Met Arg Ser		
210	215	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro		
1	5	10
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu		
20	25	30
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu		
35	40	45
Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		
50	55	60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala		

65	70	75	80
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser			
85		90	95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn			
100		105	110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser			
115		120	125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg			
130		135	140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser			
145	150	155	160
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly			
165		170	175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala			
180		185	190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu			
195		200	205
Ser Met Glu Thr Thr Met Arg Ser			
210		215	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro
1				5				10				15		
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu														
				20				25				30		
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu														
				35				40				45		
Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val														
				50				55				60		
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala														
				65				70				75		80
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser														

UQ

85	90	95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		
100	105	110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		
115	120	125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg		
130	135	140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser		
145	150	155
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly		
165	170	175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala		
180	185	190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu		
195	200	205
Ser Met Glu Thr Thr Met Arg Ser		
210	215	

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro		
1	5	10
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu		
20	25	30
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu		
35	40	45
Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		
50	55	60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala		
65	70	75
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser		
85	90	95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		

62

100	105	110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		
115	120	125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg		
130	135	140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser		
145	150	155
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly		
165	170	175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala		
180	185	190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu		
195	200	205
Ser Met Glu Thr Thr Met Arg Ser		
210	215	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 216 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro		
1	5	10
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu		
20	25	30
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu		
35	40	45
Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		
50	55	60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala		
65	70	75
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser		
85	90	95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		
100	105	110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		

63

115	120	125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg		
130	135	140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser		
145	150	155
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly		
165	170	175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala		
180	185	190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu		
195	200	205
Ser Met Glu Thr Thr Met Arg Ser		
210	215	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro
1				5				10				15		
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu														
				20				25				30		
Ser Pro Ala Gly Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu														
				35				40				45		
Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val														
				50				55				60		
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala														
				65				70				75		80
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser.														
				85				90				95		
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn														
				100				105				110		
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser														
				115				120				125		

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
 130 135 140
 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
 145 150 155 160
 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly
 165 170 175
 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
 180 185 190
 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
 195 200 205
 Ser Met Glu Thr Thr Met Arg Ser
 210 215

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
 20 25 30
 Ser Pro Ala Gly Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
 35 40 45
 Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
 50 55 60
 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
 65 70 75 80
 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
 85 90 95
 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
 100 105 110
 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
 115 120 125
 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
 130 135 140

65

His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
 145 150 155 160
 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly
 165 170 175
 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
 180 185 190
 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
 195 200 205
 Ser Met Glu Thr Thr Met Arg Ser
 210 215

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
 20 25 30
 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
 35 40 45
 Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
 50 55 60
 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
 65 70 75 80
 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
 85 90 95
 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
 100 105 110
 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
 115 120 125
 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
 130 135 140
 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
 145 150 155 160

Lele

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly
 165 170 175
 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
 180 185 190
 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
 195 200 205
 Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser
 210 215 220
 Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro
 225 230 235 240
 Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln
 245 250 255
 Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly
 260 265 270
 Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg
 275 280 285
 Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr
 290 295 300
 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp
 305 310 315 320
 Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu
 325 330 335
 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu
 340 345 350
 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His
 355 360 365
 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe
 370 375 380
 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu
 385 390 395 400
 Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu
 405 410 415
 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val
 420 425 430
 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala
 435 440 445
 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn
 450 455 460
 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr

465	470	475	480
Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg			
485	490	495	
Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr			
500	505	510	
Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu			
515	520	525	
Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr			
530	535	540	
Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys			
545	550	555	560
Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His			
565	570	575	
Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe			
580	585	590	
Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala			
595	600	605	
Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys			
610	615	620	
Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val			
625	630	635	640
Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala			
645	650	655	
Cys Met Ser Ala Asp Leu Glu Val Val Thr			
660	665		

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro
1				5				10				15		

Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu
				20			25					30			

Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		
50	55	60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala		
65	70	75
80		
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser		
85	90	95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		
100	105	110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		
115	120	125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg		
130	135	140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser		
145	150	155
160		
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly		
165	170	175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala		
180	185	190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu		
195	200	205
Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser		
210	215	220
Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro		
225	230	235
240		
Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln		
245	250	255
Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly		
260	265	270
Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg		
275	280	285
Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr		
290	295	300
Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp		
305	310	315
320		
Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu		
325	330	335
Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu		
340	345	350

Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His
 355 360 365
 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe
 370 375 380
 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu
 385 390 395 400
 Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu
 405 410 415
 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val
 420 425 430
 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala
 435 440 445
 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn
 450 455 460
 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr
 465 470 475 480
 Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg
 485 490 495
 Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr
 500 505 510
 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu
 515 520 525
 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr
 530 535 540
 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys
 545 550 555 560
 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His
 565 570 575
 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe
 580 585 590
 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala
 595 600 605
 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys
 610 615 620
 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val
 625 630 635 640
 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
 645 650 655

Cys Met Ser Ala Asp Leu Glu Val Val Thr
 660 665

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
 35 40 45

Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
 50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
 65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
 85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
 100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
 130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser
 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly
 165 170 175

Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
 180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
 195 200 205

Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser
 210 215 220

Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro
 225 230 235 240
 Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln
 245 250 255
 Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly
 260 265 270
 Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg
 275 280 285
 Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr
 290 295 300
 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp
 305 310 315 320
 Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu
 325 330 335
 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu
 340 345 350
 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His
 355 360 365
 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe
 370 375 380
 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu
 385 390 395 400
 Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu
 405 410 415
 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val
 420 425 430
 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala
 435 440 445
 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn
 450 455 460
 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr
 465 470 475 480
 Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg
 485 490 495
 Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr
 500 505 510
 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu
 515 520 525
 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr

530	535	540
Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys		
545	550	555
Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His		
565	570	575
Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe		
580	585	590
Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala		
595	600	605
Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys		
610	615	620
Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val		
625	630	635
640		
Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala		
645	650	655
Cys Met Ser Ala Asp Leu Glu Val Val Thr		
660	665	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 666 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro		
1	5	10
15		
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu		
20	25	30
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu		
35	40	45
Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		
50	55	60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala		
65	70	75
80		
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser		
85	90	95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		

100	105	110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		
115	120	125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg		
130	135	140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser		
145	150	155
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly		
165	170	175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala		
180	185	190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu		
195	200	205
Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser		
210	215	220
Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro		
225	230	235
240		
Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln		
245	250	255
Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly		
260	265	270
Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg		
275	280	285
Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr		
290	295	300
Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp		
305	310	315
320		
Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu		
325	330	335
Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu		
340	345	350
Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His		
355	360	365
Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe		
370	375	380
Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu		
385	390	395
400		
Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu		
405	410	415

Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val
 420 425 430

Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala
 435 440 445

Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn
 450 455 460

Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr
 465 470 475 480

Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg
 485 490 495

Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr
 500 505 510

Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu
 515 520 525

Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr
 530 535 540

Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys
 545 550 555 560

Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His
 565 570 575

Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe
 580 585 590

Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala
 595 600 605

Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys
 610 615 620

Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val
 625 630 635 640

Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
 645 650 655

Cys Met Ser Ala Asp Leu Glu Val Val Thr
 660 665

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear

75

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
 35 40 45

Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
 50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
 65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
 85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
 100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
 130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
 165 170 175

Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
 180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
 195 200 205

Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser
 210 215 220

Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro
 225 230 235 240

Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln
 245 250 255

Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly
 260 265 270

Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg
 275 280 285

Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr
 290 295 300
 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp
 305 310 315 320
 Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu
 325 330 335
 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu
 340 345 350
 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His
 355 360 365
 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe
 370 375 380
 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu
 385 390 395 400
 Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu
 405 410 415
 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val
 420 425 430
 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala
 435 440 445
 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn
 450 455 460
 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr
 465 470 475 480
 Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg
 485 490 495
 Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr
 500 505 510
 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu
 515 520 525
 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr
 530 535 540
 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys
 545 550 555 560
 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His
 565 570 575
 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe
 580 585 590
 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala

595	600	605
Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys		
610	615	620
Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val		
625	630	635
Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala		
645	650	655
Cys Met Ser Ala Asp Leu Glu Val Val Thr		
660	665	

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	
1				5				10					15		
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu
				20				25					30		
Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu
				35			40					45			
Leu	Gly	Cys	Lys	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val
				50			55				60				
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala
				65			70			75			80		
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser
				85				90				95			
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn
				100				105				110			
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser
				115				120				125			
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg
				130			135				140				
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	
				145			150			155			160		
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	Gly

165	170	175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala		
180	185	190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu		
195	200	205
Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser		
210	215	220
Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro		
225	230	235
Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln		
245	250	255
Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly		
260	265	270
Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg		
275	280	285
Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr		
290	295	300
Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp		
305	310	315
320		
Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu		
325	330	335
Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu		
340	345	350
Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His		
355	360	365
Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe		
370	375	380
Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu		
385	390	395
400		
Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu		
405	410	415
Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val		
420	425	430
Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala		
435	440	445
Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn		
450	455	460
Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr		
465	470	475
480		

Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg
 485 490 495

Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr
 500 505 510

Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu
 515 520 525

Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr
 530 535 540

Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys
 545 550 555 560

Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His
 565 570 575

Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe
 580 585 590

Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala
 595 600 605

Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys
 610 615 620

Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val
 625 630 635 640

Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
 645 650 655

Cys Met Ser Ala Asp Leu Glu Val Val Thr
 660 665

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
 35 40 45

86

Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
 50 55 60

 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
 65 70 75 80

 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
 85 90 95

 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
 100 105 110

 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
 115 120 125

 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
 130 135 140

 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
 145 150 155 160

 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
 165 170 175

 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
 180 185 190

 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
 195 200 205

 Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser
 210 215 220

 Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro
 225 230 235 240

 Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln
 245 250 255

 Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly
 260 265 270

 Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg
 275 280 285

 Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr
 290 295 300

 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp
 305 310 315 320

 Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu
 325 330 335

 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu
 340 345 350

Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His
 355 360 365
 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe
 370 375 380
 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu
 385 390 395 400
 Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu
 405 410 415
 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val
 420 425 430
 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala
 435 440 445
 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn
 450 455 460
 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr
 465 470 475 480
 Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg
 485 490 495
 Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr
 500 505 510
 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu
 515 520 525
 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr
 530 535 540
 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys
 545 550 555 560
 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His
 565 570 575
 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe
 580 585 590
 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala
 595 600 605
 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys
 610 615 620
 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val
 625 630 635 640
 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
 645 650 655
 Cys Met Ser Ala Asp Leu Glu Val Val Thr

660

665

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	
1				5										15	
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu
				20				25						30	
Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu
				35				40						45	
Leu	Gly	Cys	Lys	Lys	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val
				50				55						60	
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala
				65				70						80	
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser
				85					90					95	
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn
				100				105						110	
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser
				115				120						125	
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg
				130				135						140	
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	
				145				150						160	
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	
				165					170					175	
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala
				180				185						190	
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu
				195				200						205	
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser
				210				215						220	
Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro

83

225	230	235	240
Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln			
245	250	255	
Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly			
260	265	270	
Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg			
275	280	285	
Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr			
290	295	300	
Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp			
305	310	315	320
Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu			
325	330	335	
Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu			
340	345	350	
Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His			
355	360	365	
Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe			
370	375	380	
Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu			
385	390	395	400
Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu			
405	410	415	
Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val			
420	425	430	
Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala			
435	440	445	
Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn			
450	455	460	
Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr			
465	470	475	480
Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg			
485	490	495	
Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr			
500	505	510	
Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu			
515	520	525	
Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr			
530	535	540	

Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys
545					550				555						560
Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His
					565				570						575
Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe
					580			585							590
Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala
					595			600				605			
Pro	Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys
					610			615				620			
Pro	Thr	Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val
					625			630			635				640
Gln	Asn	Glu	Val	Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala
					645				650						655
Cys	Met	Ser	Ala	Asp	Leu	Glu	Val	Val	Thr						
					660				665						

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	
1				5					10				15		
Arg	Gly	Ser	His	Met	Ala	Tyr	Ser	Leu	Thr	Thr	Gly	Ser	Val	Val	Ile
					20				25				30		
Val	Gly	Arg	Ile	Ile	Leu	Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser
					35			40				45			
Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly
					50			55			60				
Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala
					65			70			75				80
Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val
					85				90				95		
Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile
					100				105				110		

Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala
 115 120 125

Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp
 130 135 140

Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg
 145 150 155 160

Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu
 165 170 175

Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala Val
 180 185 190

Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val
 195 200 205

Asp Phe Val Pro Val Glu Ser Met Glu Thr Thr Met Arg Ser Pro Val
 210 215 220

Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Pro Gln Ser Phe Gln Val
 225 230 235 240

Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro
 245 250 255

Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser
 260 265 270

Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly
 275 280 285

Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ala
 290 295 300

Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys
 305 310 315 320

Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr
 325 330 335

Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu
 340 345 350

Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly
 355 360 365

Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Asn
 370 375 380

Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile
 385 390 395 400

Arg Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp
 405 410 415

Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr
 420 425 430
 Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val
 435 440 445
 Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp
 450 455 460
 Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser
 465 470 475 480
 Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp Ala
 485 490 495
 Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Gly
 500 505 510
 Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe Asp
 515 520 525
 Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu
 530 535 540
 Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr
 545 550 555 560
 Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val
 565 570 575
 Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys
 580 585 590
 Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val
 595 600 605
 Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys
 610 615 620
 Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu
 625 630 635 640
 Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile
 645 650 655
 Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val Thr
 660 665 670

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 672 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15

Arg Gly Ser His Met Ala Tyr Ser Leu Thr Thr Gly Ser Val Val Ile
 20 25 30

Val Gly Arg Ile Ile Leu Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser
 35 40 45

Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly
 50 55 60

Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala
 65 70 75 80

Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val
 85 90 95

Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile
 100 105 110

Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala
 115 120 125

Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp
 130 135 140

Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg
 145 150 155 160

Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu
 165 170 175

Lys Gly Ser Ala Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala Val
 180 185 190

Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val
 195 200 205

Asp Phe Val Pro Val Glu Ser Met Glu Thr Thr Met Arg Ser Pro Val
 210 215 220

Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Pro Gln Ser Phe Gln Val
 225 230 235 240

Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro
 245 250 255

Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser
 260 265 270

Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly
 275 280 285

Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ala

290	295	300
Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys		
305	310	315
Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr		
325	330	335
Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu		
340	345	350
Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly		
355	360	365
Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Asn		
370	375	380
Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile		
385	390	395
Arg Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp		
405	410	415
Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr		
420	425	430
Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val		
435	440	445
Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp		
450	455	460
Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser		
465	470	475
Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp Ala		
485	490	495
Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly		
500	505	510
Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe Asp		
515	520	525
Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu		
530	535	540
Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr		
545	550	555
Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val		
565	570	575
Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys		
580	585	590
Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val		
595	600	605

Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys
 610 615 620

Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu
 625 630 635 640

Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile
 645 650 655

Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val Thr
 660 665 670

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Ser Gly Ser
 1

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Pro Ala Gly Gly
 1

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 632 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Ala Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly
 1 5 10 15

Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly
 20 25 30

Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys
 35 40 45

Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr
 50 55 60

Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp
 65 70 75 80

Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr
 85 90 95

Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
 100 105 110

Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
 115 120 125

Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
 130 135 140

Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys
 145 150 155 160

Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met
 165 170 175

Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro
 180 185 190

Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly
 195 200 205

Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr
 210 215 220

Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly
 225 230 235 240

Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly
 245 250 255

Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly
 260 265 270

Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile

91

275

280

285

Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile
 290 295 300

Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val
 305 310 315 320

Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn
 325 330 335

Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly
 340 345 350

Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Arg His Leu Ile Phe
 355 360 365

Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly
 370 375 380

Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val
 385 390 395 400

Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met
 405 410 415

Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys
 420 425 430

Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu
 435 440 445

Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly
 450 455 460

Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly
 465 470 475 480

Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr
 485 490 495

Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val
 500 505 510

Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp
 515 520 525

His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp
 530 535 540

Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr
 545 550 555 560

Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro
 565 570 575

Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr
 580 585 590

Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn
 595 600 605

Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met
 610 615 620

Ser Ala Asp Leu Glu Val Val Thr
 625 630

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr
 1 5 10 15

Cys Leu Thr Thr Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu Ser
 20 25 30

Gly Arg Pro Ala Ile Val Pro Asp Arg Glu Leu Leu Tyr Gln Glu Phe
 35 40 45

Asp Glu Met Glu Glu Cys
 50

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp Thr Glu Asp Val Val Cys Cys Ser Met Tyr Thr Trp Thr Gly Lys
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTGG TAGTGGTAGT	60
ATCACGGCCT ACTCCCAA	78

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT	36
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(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC	39
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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

94

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCCTGTAAAGG CTAGTCTTCT TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCCTACTTG AAGGGCTCTG CTGGTGGTCC ACTGCTCTGC

40

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCAGAGCACT GGACCACCAAG CAGAGCCCTT CAAGTAGGAG

40

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

96

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCCTGTAAAGG CTAGTGATCT TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTCC TGCTGGTGGT

60

ATCACGGCCT ACTCCCAA

78

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT

36

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCCTGTAAAGG CTAGTGATCT TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

99

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
 20 25 30

Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu
 35 40 45

Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu
 50 55 60

Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr
 65 70 75 80

Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys
 85 90 95

Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val
 100 105 110

Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu
 115 120 125

Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His
 130 135 140

Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu
 145 150 155 160

Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro
 165 170 175

Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val
 180 185 190

Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser
 195 200 205

Met Glu Thr Thr Met Arg Ser
 210 215

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Pro Ala Gly
1

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTCC TGCTGGTATC	60
ACGGCCTACT CCCAA	75

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT	36
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(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 215 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

101

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
 20 25 30

Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu
 35 40 45

Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu
 50 55 60

Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr
 65 70 75 80

Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys
 85 90 95

Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val
 100 105 110

Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu
 115 120 125

Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His
 130 135 140

Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu
 145 150 155 160

Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro
 165 170 175

Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val
 180 185 190

Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser
 195 200 205

Met Glu Thr Thr Met Arg Ser
 210 215

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCCTGTAAAGG CTAGTGATCT TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro
1				5										15

Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu
				20					25					30	

Ser	Gly	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu
				35				40				45			

Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glut
				50			55				60				

Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr
				65			70		75					80	

Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys
					85			90					95		

Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val
				100				105				110			

Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu
					115			120				125			

Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His
					130			135			140				

Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu
 145 150 155 160

Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro
 165 170 175

Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val
 180 185 190

Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser
 195 200 205

Met Glu Thr Thr Met Arg Ser
 210 215

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Gly Ser
 1

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAACCA TTTTATCTGG TGGTTCTATC 60
 ACGGCCTACT CCCAA 75

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT

36

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
20 25 30

Ser Gly Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu
35 40 45

Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu
50 55 60

Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr
65 70 75 80

Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys
85 90 95

Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val
100 105 110

Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu
115 120 125

Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His
130 135 140

Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu
145 150 155 160

Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro
165 170 175

165

Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val
 180 185 190

Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser
 195 200 205

Met Glu Thr Thr Met Arg Ser
 210 215

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 646 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met His Met His His His His His Leu Val Pro Arg Gly Ser Ala
 1 5 10 15

Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Lys

106

20	25	30
Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val		
35	40	45
Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn		
50	55	60
Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala		
65	70	75
Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp		
85	90	95
Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys		
100	105	110
Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val		
115	120	125
Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro		
130	135	140
Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys		
145	150	155
Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg		
165	170	175
Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr		
180	185	190
Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val		
195	200	205
Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly		
210	215	220
Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val		
225	230	235
Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr		
245	250	255
Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg		
260	265	270
Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe		
275	280	285
Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys		
290	295	300
Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr		
305	310	315
Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala		
325	330	335

Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu
 340 345 350
 Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala
 355 360 365
 Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His
 370 375 380
 Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly
 385 390 395 400
 Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro
 405 410 415
 Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met Thr Gly
 420 425 430
 Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr
 435 440 445
 Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr
 450 455 460
 Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr
 465 470 475 480
 Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg
 485 490 495
 Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala
 500 505 510
 Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu
 515 520 525
 Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu
 530 535 540
 Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His
 545 550 555 560
 Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val
 565 570 575
 Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser
 580 585 590
 Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His
 595 600 605
 Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val
 610 615 620
 Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala
 625 630 635 640

Asp Leu Glu Val Val Thr
645

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 646 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met His Met His His His His His His	Leu Val Pro Arg Gly Ser Ala		
1	5	10	15

Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile		
20	25	30

Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val

109

35	40	45
Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn		
50	55	60
Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala		
65	70	75
Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp		
85	90	95
Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys		
100	105	110
Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val		
115	120	125
Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro		
130	135	140
Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys		
145	150	155
160		
Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg		
165	170	175
Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr		
180	185	190
Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val		
195	200	205
Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly		
210	215	220
Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val		
225	230	235
240		
Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr		
245	250	255
Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg		
260	265	270
Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe		
275	280	285
Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys		
290	295	300
Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr		
305	310	315
320		
Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala		
325	330	335
Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu		
340	345	350

Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala
 355 360 365
 Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His
 370 375 380
 Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly
 385 390 395 400
 Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro
 405 410 415
 Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met Thr Gly
 420 425 430
 Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr
 435 440 445
 Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr
 450 455 460
 Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr
 465 470 475 480
 Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg
 485 490 495
 Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala
 500 505 510
 Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu
 515 520 525
 Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu
 530 535 540
 Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His
 545 550 555 560
 Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val
 565 570 575
 Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser
 580 585 590
 Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His
 595 600 605
 Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val
 610 615 620
 Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala
 625 630 635 640
 Asp Leu Glu Val Val Thr
 645

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met His Met His His His His His Leu Val Pro Arg Gly Ser Ala
 1 5 10 15

Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile
 20 25 30

Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val
 35 40 45

Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn
 50 55 60

Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala
 65 70 75 80

Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp
 85 90 95

Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys
 100 105 110

Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val
 115 120 125

Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro
 130 135 140

Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly Pro Leu Leu Cys
 145 150 155 160

Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg
 165 170 175

Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr
 180 185 190

Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val
 195 200 205

Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly
 210 215 220

Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val
 225 230 235 240

Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr
 245 250 255

Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg
 260 265 270

Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe
 275 280 285

Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys
 290 295 300

Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr
 305 310 315 320

Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala
 325 330 335

Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu
 340 345 350

Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala
 355 360 365

Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His
 370 375 380

Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly
 385 390 395 400

Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro
 405 410 415

Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met Thr Gly
 420 425 430

Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr
 435 440 445

Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr
 450 455 460

Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr
 465 470 475 480

Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg
 485 490 495

Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala
 500 505 510

Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu
 515 520 525

Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu
 530 535 540

Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His
 545 550 555 560

Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val
 565 570 575

Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser
 580 585 590

Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His
 595 600 605

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val
 610 615 620

Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala
 625 630 635 640

Asp Leu Glu Val Val Thr
 645

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs

114

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTCCTACTTG AAGGGCTCTG CTGGTGGTCC ACTGCTCTGC

40

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCAGAGGAGT GGACCACCAAG CAGAGCCCTT CAAGTAGGAG

40

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 646 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met His Met His His His His His Leu Val Pro Arg Gly Ser Ala
 1 5 10 15

Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile
 20 25 30

Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val
 35 40 45

Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn
 50 55 60

Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala
 65 70 75 80

115

385	390	395	400
Ile Asn Ala Val Ala	Tyr Tyr Arg Gly	Leu Asp Val Ser Val	Ile Pro
405		410	415
Thr Ser Gly Asp Val Val Val	Ala Thr Asp Ala	Leu Met Thr Gly	
420	425	430	
Tyr Thr Gly Asp Phe Asp Ser Val	Ile Asp Cys Asn Thr Cys Val Thr		
435	440	445	
Gln Thr Val Asp Phe Ser	Leu Asp Pro Thr Phe Thr	Ile Glu Thr Thr	
450	455	460	
Thr Val Pro Gln Asp Ala Val Ser Arg Ser	Gln Arg Arg Gly Arg	Thr	
465	470	475	480
Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg			
485	490	495	
Pro Ser Gly Met Phe Asp Ser Ser Val	Leu Cys Glu Cys Tyr Asp Ala		
500	505	510	
Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu			
515	520	525	
Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu			
530	535	540	
Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His			
545	550	555	560
Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val			
565	570	575	
Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser			
580	585	590	
Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His			
595	600	605	
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val			
610	615	620	
Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala			
625	630	635	640
Asp Leu Glu Val Val Thr			
645			

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTCCGTCATA CCAACTTCCG GAGACGTCGT TGTCT

35

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CGACAACGAC GTCTCCGGAA GTTGGTATGA CGGAC

35

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met His Met His His His His His Leu Val Pro Arg Gly Ser Ala
 1 5 10 15

Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile
 20 25 30

Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val
 35 40 45

Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn
 50 55 60

Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala
 65 70 75 80

Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp
 85 90 95

Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys
 100 105 110
 Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val
 115 120 125
 Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro
 130 135 140
 Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys
 145 150 155 160
 Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg
 165 170 175
 Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr
 180 185 190
 Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val
 195 200 205
 Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly
 210 215 220
 Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val
 225 230 235 240
 Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr
 245 250 255
 Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg
 260 265 270
 Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe
 275 280 285
 Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys
 290 295 300
 Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr
 305 310 315 320
 Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala
 325 330 335
 Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu
 340 345 350
 Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala
 355 360 365
 Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His
 370 375 380
 Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly
 385 390 395 400
 Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro

405	410	415
Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly		
420	425	430
Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr		
435	440	445
Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr		
450	455	460
Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr		
465	470	475
Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg		
485	490	495
Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala		
500	505	510
Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu		
515	520	525
Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu		
530	535	540
Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His		
545	550	555
Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val		
565	570	575
Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser		
580	585	590
Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His		
595	600	605
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val		
610	615	620
Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala		
625	630	635
Asp Leu Glu Val Val Thr		
645		

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACTAAAGTGC CGGCTGCCTA CGCAGCCCAA GGG

33

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CCCTTGGGCT GCGTAGGCAG CCGGCACCTT AGT

33

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GCCTGTAAAGG CTAGTGATCT TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:77:

121

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGG

38

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

122

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GCCTGTAAGG CTAGTCTTCT TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

123

CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GCCTGTAAGG CTAGTCTTCT TGCAACCAAG TAGGCCCG

39

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid

124

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GATATACATA TGGCTTACTC TCTGACTACG GGTTCTGTTG TTATTGTTGG TAGAATTATT	60
TTATCTGGTA GTGGTAGTAT CACGGCCTAC TCCCAA	96

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTGGTGGTGC TCGAGGCTGC CGCGCGGCAC CAGCGTAACG ACCTCCAGGT C	51
--	----

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GATATACATA TGGCTTACTC TCTGACTACG GGTTCTGTTG TTATTGTTGG TAGAATTATT	60
TTATCTGGTA GTGGTAGTAT CACGGCCTAC TCCCAA	96

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGGTGGTGCT CGAGGCTGCC GCGCGGCACC AGCGTAACGA CCTCCAGGTC

50

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Asp	Thr	Glu	Asp	Val	Val	Ala	Cys	Ser	Met	Ser	Tyr	Thr	Trp	Tyr	Gly
1				5					10					15	

Lys

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATG	GGC	AGC	AGC	CAT	CAT	CAT	CAT	CAC	AGC	AGC	GGC	CTG	GTG	CCG		
Met	Gly	Ser	Ser	His	Ser	Ser	Gly	Leu	Val	Pro						
1				5							10			15		

48

CGC	GGC	AGC	CAT	ATG	GGT	TCT	GTT	ATT	GTT	GGT	AGA	ATT	ATT	TTA		
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu	
				20				25					30			

96

TCT	GGT	AGT	GGT	AGT	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	CTA	
Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	

144

126

35	40	45	
CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	50	55	192
50	55	60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	65	70	240
65	70	75	80
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	85	90	288
85	90	95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	100	105	336
100	105	110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	115	120	384
115	120	125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	130	135	432
130	135	140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	145	150	480
145	150	155	160
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly	165	170	528
165	170	175	
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	180	185	576
180	185	190	
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	195	200	624
195	200	205	
TCC ATG GAA ACT ACT ATG CGG TCT TGA Ser Met Glu Thr Thr Met Arg Ser	210	215	651
210	215		

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

127

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATG	GGC	AGC	AGC	CAT	CAT	CAT	CAT	CAC	AGC	AGC	GGC	CTG	GTG	CCG	48	
Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Ieu	Val	Pro	
1		5						10					15			
CGC	GGC	AGC	CAT	ATG	GGT	TCT	GTT	ATT	GTT	GGT	AGA	ATT	ATT	TTA	96	
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	
				20			25				30					
TCT	GGT	AGT	GGT	AGT	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	CTA	144
Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Ieu	
				35			40				45					
CTT	GGT	TGC	AAG	ATC	ACT	AGC	CTT	ACA	GGC	CGG	GAC	AAG	AAC	CAG	GTC	192
Leu	Gly	Cys	Lys	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	
				50			55				60					
GAG	GGA	GAG	GTT	CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	240
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	
				65			70				75		80			
ACC	TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	288
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	
				85			90				95					
AAG	ACC	TTA	GCC	GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	336
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	
				100			105				110					
GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	384
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	
				115			120				125					
TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	432
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	
				130			135				140					
CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GAC	AGT	AGG	GGG	AGC	480	
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	
				145			150				155		160			
CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	528
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	
				165			170				175					
CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	576
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	
				180			185				190					
GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	624
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	
				195			200				205					

128

TCC ATG GAA ACT ACT ATG CGG TCT TGA
 Ser Met Glu Thr Thr Met Arg Ser
 210 215

651

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC ATC AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	

129

CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160	480
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly 165 170 175	528
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190	576
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205	624
TCC ATG GAA ACT ACT ATG CGG TCT TGA Ser Met Glu Thr Thr Met Arg Ser 210 215	651

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro 1 5 10 15	48
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30	96
TCT GGT AGT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45	144
CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 50 55 60	192
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240

30

Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	
65					70					75					80	
ACC	TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	288
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	
					85				90					95		
AAG	ACC	TTA	GCC	GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	336
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	
					100				105					110		
GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	384
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	
					115				120					125		
TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	432
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	
					130				135					140		
CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	480
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	
					145				150					160		
CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	528
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	
					165				170					175		
CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	576
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	
					180				185					190		
GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	624
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	
					195				200					205		
TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	TGA								651
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser									
					210				215							

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	1	5	10	15	48
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	20	25	30		96
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	35	40	45		144
CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	50	55	60		192
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	65	70	75	80	240
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	85	90	95		288
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	100	105	110		336
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	115	120	125		384
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	130	135	140		432
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	145	150	155	160	480
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly	165	170	175		528
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	180	185	190		576
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	195	200	205		624
TCC ATG GAA ACT ACT ATG CGG TCT TGA Ser Met Glu Thr Thr Met Arg Ser	210	215			651

(2) INFORMATION FOR SEQ ID NO:97:

132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
145 150 155 160	
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT	528

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Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	Gly	
165									170						175	
CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	576
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	
180									185						190	
GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	624
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	
195									200						205	
TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	TGA								651
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser									
210							215									

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATG	GGC	AGC	AGC	CAT	CAT	CAT	CAT	CAC	AGC	AGC	GGC	CTG	GTG	CCG		48
Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro		
1				5					10				15			
CGC	GGC	AGC	CAT	ATG	GGT	TCT	GTT	ATT	GTT	GGT	AGA	ATT	ATT	TTA		96
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu	
				20				25						30		
TCT	GGT	AGT	GGT	AGT	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	CTA	144
Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	
					35			40				45				
CTT	GGT	TGC	ATC	AAG	ACT	AGC	CTT	ACA	GGC	CGG	GAC	AAG	AAC	CAG	GTC	192
Leu	Gly	Cys	Ile	Lys	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	
				50			55				60					
GAG	GGA	GAG	GTT	CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	240
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	
				65			70				75			80		
ACC	TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	288
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	
					85				90				95			

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AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110	336
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125	384
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140	432
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160	480
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly 165 170 175	528
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190	576
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205	624
TCC ATG GAA ACT ACT ATG CGG TCT TGA Ser Met Glu Thr Thr Met Arg Ser 210 215	651

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro 1 5 10 15	48
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	96

135

20	25	30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu			144
35	40	45	
CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val			192
50	55	60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala			240
65	70	75	80
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser			288
85	90	95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn			336
100	105	110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser			384
115	120	125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg			432
130	135	140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser			480
145	150	155	160
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly			528
165	170	175	
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala			576
180	185	190	
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu			624
195	200	205	
TCC ATG GAA ACT ACT ATG CGG TCT TGA Ser Met Glu Thr Thr Met Arg Ser			651
210	215		

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

136

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT CCT GCT GGT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Pro Ala Gly Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
G TG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
145 150 155 160	
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT	528
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly	
165 170 175	
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	
180 185 190	

GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG 624
 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
 195 200 205

TCC ATG GAA ACT ACT ATG CGG TCT TGA 651
 Ser Met Glu Thr Thr Met Arg Ser
 210 215

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48
 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15

CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA 96
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
 20 25 30

TCT CCT GCT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144
 Ser Pro Ala Gly Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
 35 40 45

CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC 192
 Leu Gly Cys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
 50 55 60

GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG 240
 Glu Gly Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
 65 70 75 80

ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA 288
 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
 85 90 95

AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT 336
 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
 100 105 110

GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC 384
 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser

138

CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 50 55 60	192
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 65 70 75 80	240
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95	288
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110	336
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125	384
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140	432
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160	480
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly 165 170 175	528
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190	576
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205	624
TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser 210 215 220	672
CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro 225 230 235 240	720
ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln 245 250 255	768
GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 260 265 270	816
TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg	864

140

115	120	125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130	135	140	432
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145	150	155	480
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly 165	170	175	528
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CCG GCT GCC Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180	185	190	576
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195	200	205	624
TCC ATG GAA ACT ACT ATG CGG TCT TGA Ser Met Glu Thr Thr Met Arg Ser 210	215		651

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro 1	5	10	48
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20	25	30	96
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35	40	45	144

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275	280	285	
ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr	290	295	912
290	295	300	
TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp	305	310	960
305	310	315	320
ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu	325	330	1008
325	330	335	
GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu	340	345	1056
340	345	350	
GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His	355	360	1104
355	360	365	
CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe	370	375	1152
370	375	380	
TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu	385	390	1200
385	390	395	400
ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu	405	410	1248
405	410	415	
TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val	420	425	1296
420	425	430	
TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala	435	440	1344
435	440	445	
CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn	450	455	1392
450	455	460	
ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr	465	470	1440
465	470	475	480
ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg	485	490	1488
485	490	495	
CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr	500	505	1536
500	505	510	

1481

CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 515 520 525	1584
TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 540	1632
TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 555 560	1680
CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 570 575	1728
ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590	1776
CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 605	1824
CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 620	1872
CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 640	1920
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 645 650 655	1968
TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT Cys Met Ser Ala Asp Leu Glu Val Val Thr 660 665	1998

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1998 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1998

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser	
145 150 155 160	
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT	528
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly	
165 170 175	
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	
180 185 190	
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG	624
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	
195 200 205	
TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC	672
Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser	
210 215 220	

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CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro 225 230 235 240	720
ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln 245 250 255	768
GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 260 265 270	816
TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg 275 280 285	864
ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 290 295 300	912
TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 305 310 315 320	960
ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325 330 335	1008
GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 340 345 350	1056
GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 355 360 365	1104
CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 370 375 380	1152
TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385 390 395 400	1200
ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 410 415	1248
TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 430	1296
TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala 435 440 445	1344
CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn	1392

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450	455	460	
ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr	465	470	480
475	480		
ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg	485	490	495
CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr	500	505	510
CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu	515	520	525
TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr	530	535	540
TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys	545	550	560
CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His	565	570	575
ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe	580	585	590
CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala	595	600	605
CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys	610	615	620
CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val	625	630	640
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala	645	650	655
TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT Cys Met Ser Ala Asp Leu Glu Val Val Thr	660	665	1998

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

145

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	48
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	96
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	144
35 40 45	
CTT GGT TGC ATC AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	192
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	240
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	288
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	336
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	384
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	432
130 135 140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser	480
145 150 155 160	
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly	528

176

165	170	175	
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180	185	190	576
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195	200	205	624
TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser 210	215	220	672
CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro 225	230	235	720
ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln 245	250	255	768
GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 260	265	270	816
TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg 275	280	285	864
ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 290	295	300	912
TAT GGC AAG TTT CTT GCC GAT GGT TGC TCT GGG GGC GCT TAT GAC Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 305	310	315	960
ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325	330	335	1008
GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 340	345	350	1056
GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 355	360	365	1104
CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 370	375	380	1152
TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385	390	395	1200

ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 410 415	1248
TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 430	1296
TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala 435 440 445	1344
CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 460	1392
ACA TGT GTC ACC' CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 465 470 475 480	1440
ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 . 490 495	1488
CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 500 505 510	1536
CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 515 520 525	1584
TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 540	1632
TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 555 560	1680
CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 570 575	1728
ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590	1776
CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 605	1824
CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 . 620	1872
CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val	1920

148

625	630	635	640	
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala				1968
645 650 655				
TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT Cys Met Ser Ala Asp Leu Glu Val Val Thr				1998
660 665				

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	

146

GTC GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125	384
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140	432
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160	480
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly 165 170 175	528
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190	576
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205	624
TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser 210 215 220	672
CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro 225 230 235 240	720
ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln 245 250 255	768
GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 260 265 270	816
TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg 275 280 285	864
ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 290 295 300	912
TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 305 310 315 320	960
ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325 330 335	1008
GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu	1056

150

340	345	350	
GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His			1104
355 360 365			
CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe			1152
370 375 380			
TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu			1200
385 390 395 400			
ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu			1248
405 410 415			
TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val			1296
420 425 430			
TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala			1344
435 440 445			
CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn			1392
450 455 460			
ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr			1440
465 470 475 480			
ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg			1488
485 490 495			
CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr			1536
500 505 510			
CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu			1584
515 520 525			
TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr			1632
530 535 540			
TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys			1680
545 550 555 560			
CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His			1728
565 570 575			

ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590	1776
CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 605	1824
CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 620	1872
CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 640	1920
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 645 650 655	1968
TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT Cys Met Ser Ala Asp Leu Glu Val Val Thr 660 665	1998

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1998 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro 1 5 10 15	48
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30	96
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45	144
CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 50 55 60	192

GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 65 70 75 80	240
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95	288
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110	336
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125	384
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140	432
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160	480
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly 165 170 175	528
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190	576
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205	624
TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser 210 215 220	672
CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro 225 230 235 240	720
ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln 245 250 255	768
GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 260 265 270	816
TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg 275 280 285	864
ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC	912

153

Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	
290						295					300					
TAT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	960
Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	
305						310				315				320		
ATC	ATA	ATA	TGT	GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	1008
Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	
							325			330			335			
GGC	ATC	GGC	ACA	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	1056
Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	
							340		345			350				
GTC	GTG	CTC	GCC	ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	1104
Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	
							355		360			365				
CCA	AAC	ATC	GAG	GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	1152
Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	
							370		375			380				
TAT	GGC	AAA	GCC	ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGG	AGG	CAT	CTC	1200
Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	
							385		390		395		400			
ATT	TTC	TGT	CAT	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	1248
Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	
							405		410			415				
TCA	GGC	CTC	GGA	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	1296
Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	
							420		425			430				
TCC	GTC	ATA	CCA	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	1344
Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	
							435		440			445				
CTG	ATG	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	1392
Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	
							450		455			460				
ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	1440
Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	
							465		470		475		480			
ATT	GAG	ACG	ACG	ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG	1488
Ile	Glu	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg		
							485		490			495				
CGG	GGT	AGG	ACT	GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT	1536
Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	
							500		505			510				
CCG	GGA	GAA	CGG	CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG	1584
Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	
							515		520			525				

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TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 540	1632
TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 555 560	1680
CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 570 575	1728
ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590	1776
CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 605	1824
CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 620	1872
CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 640	1920
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 645 650 655	1968
TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT Cys Met Ser Ala Asp Leu Glu Val Val Thr 660 665	1998

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1998 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG
Met Gly Ser Ser His His His His Ser Ser Gly Leu Val Pro

155

1	5	10	15	
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	20 .	25	30	96
TCT GGT AGT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	35	40	45	144
CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	50	55	60	192
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	65	70	75	240
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	85	90	95	288
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	100	105	110	336
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	115	120	125	384
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	130	135	140	432
CAT GCT GAC GTC ATT CCG GTG CGC CCG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	145	150	155	480
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly	165	170	175	528
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CCG GCT GCC Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	180	185	190	576
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	195	200	205	624
TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser	210	215 .	220	672
CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro	225	230	235	720

156

ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln 245 250 255	768
GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 260 265 270	816
TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg 275 280 285	864
ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 290 295 300	912
TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 305 310 315 320	960
ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325 330 335	1008
GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 340 345 350	1056
GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 355 360 365	1104
CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 370 375 380	1152
TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385 390 395 400	1200
ATT TTC TGT CAT TCC AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 410 415	1248
TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 430	1296
TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala 435 440 445	1344
CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 460	1392
ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr	1440

465	470	475	480	
ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg				1488
485	490	495		
CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr				1536
500	505	510		
CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu				1584
515	520	525		
TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr				1632
530	535	540		
TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys				1680
545	550	555	560	
CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His				1728
565	570	575		
ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe				1776
580	585	590		
CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala				1824
595	600	605		
CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys				1872
610	615	620		
CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val				1920
625	630	635	640	
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala				1968
645	650	655		
TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT Cys Met Ser Ala Asp Leu Glu Val Val Thr				1998
660	665			

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1998 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

158

(D) TOPOLOGY: linear

(i) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CD

(B) LOCATION: 1..1998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC ATC AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
145 150 155 160	
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT	528
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly	
165 170 175	
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576

159

Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala			
180	185	190	
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG			624
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu			
195	200	205	
TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC			672
Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser			
210	215	220	
CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC			720
Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro			
225	230	235	240
ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA			768
Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln			
245	250	255	
GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG			816
Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly			
260	265	270	
TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA			864
Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg			
275	280	285	
ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC			912
Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr			
290	295	300	
TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC			960
Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp			
305	310	315	320
ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG			1008
Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu			
325	330	335	
GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT			1056
Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu			
340	345	350	
GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC			1104
Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His			
355	360	365	
CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC			1152
Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe			
370	375	380	
TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC			1200
Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu			
385	390	395	400
ATT TTC TGT CAT TCC AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG			1248
Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu			
405	410	415	

TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 430	1296
TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala 435 440 445	1344
CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 460	1392
ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 465 470 475 480	1440
ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 490 495	1488
CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 500 505 510	1536
CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 515 520 525	1584
TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 540	1632
TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 555 560	1680
CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 570 575	1728
ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590	1776
CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 605	1824
CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 620	1872
CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 640	1920
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA	1968

Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
645 650 655

TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT
 Cys Met Ser Ala Asp Leu Glu Val Val Thr
 660 665

1998

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

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ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG      48
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
   1           5           10          .         15

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CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
 20 25 30

TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG .ACG CGG GGC CTA 144
 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
 35 40 45

CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC
 Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
 50 55 60

GAG	GGA	GAG	GTT	CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	240
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	
65		70					75						80			

ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA
 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
 85 90 95

AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336	
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		
100	105	110

GTC GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC 384
 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
 115 120 125

TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140	432
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160	480
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly 165 170 175	528
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190	576
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205	624
TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser 210 215 220	672
CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro 225 230 235 240	720
ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln 245 250 255	768
GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 260 265 270	816
TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg 275 280 285	864
ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 290 295 300	912
TAT GGC AAG TTT CTT GCC GAT GGT TGC TCT GGG GGC GCT TAT GAC Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 305 310 315 320	960
ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325 330 335	1008
GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 340 345 350	1056
GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His	1104

355	360	365	
CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 370 375 380			1152
TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385 390 395 400			1200
ATT TTC TGT CAT TCC AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 410 415			1248
TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 430			1296
TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala 435 440 445			1344
CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 460			1392
ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 465 470 475 480			1440
ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 490 495			1488
CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 500 505 510			1536
CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 515 520 525			1584
TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 540			1632
TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 555 560			1680
CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 570 575			1728
ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590			1776

164

CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 605	1824
CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 620	1872
CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 640	1920
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 645 650 655	1968
TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT Cys Met Ser Ala Asp Leu Glu Val Val Thr 660 665	1998

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2016 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..2016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro 1 5 10 15	48
CGC GGC AGC CAT ATG GCT TAC TCT CTG ACT ACG GGT TCT GTT ATT Arg Gly Ser His Met Ala Tyr Ser Leu Thr Thr Gly Ser Val Val Ile 20 25 30	96
GTT GGT AGA ATT ATT TTA TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC Val Gly Arg Ile Ile Leu Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser 35 40 45	144
CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly 50 55 60	192
CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA	240

165

Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala				
65	70	75	80	
ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT				288
Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val				
85	90	95		
TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC				336
Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile				
100	105	110		
ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG				384
Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala				
115	120	125		
CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC				432
Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp				
130	135	140		
CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG				480
Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg				
145	150	155	160	
GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG				528
Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu				
165	170	175		
AAG GGC TCT TCG GGT GGT CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG				576
Lys Gly Ser Ser Gly Pro Leu Leu Cys Pro Ser Gly His Ala Val				
180	185	190		
GGC ATC TTC CGG GCT GCC GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG				624
Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val				
195	200	205		
GAC TTT GTG CCC GTA GAG TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC				672
Asp Phe Val Pro Val Glu Ser Met Glu Thr Thr Met Arg Ser Pro Val				
210	215	220		
TTC ACG GAC AAC TCA TCC CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG				720
Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Pro Gln Ser Phe Gln Val				
225	230	235	240	
GCC CAC CTA CAC GCT CCC ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG				768
Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro				
245	250	255		
GCT GCA TAT GCA GCC CAA GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC				816
Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser				
260	265	270		
GTT GCC GCT ACC TTA GGG TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT				864
Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly				
275	280	285		
ATT GAC CCC AAC ATC AGA ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC				912
Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ala				
290	295	300		

CCC GTC ACA TAC TCT ACC TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys 305 310 315 320	960
TCT GGG GGC GCT TAT GAC ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr 325 330 335	1008
GAC TCG ACT ACA ATC TTG GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu 340 345 350	1056
ACG GCT GGA GCG CGG CTT GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly 355 360 365	1104
TCG GTC ACC GTG CCA CAC CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Asn 370 375 380	1152
ACT GGA GAG ATC CCC TTC TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile 385 390 395 400	1200
AGG GGG GGA AGG CAT CTC ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC Arg Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp 405 410 415	1248
GAG CTC GCC GCA AAG CTG TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr 420 425 430	1296
TAC CGG GGG CTC GAT GTG TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val 435 440 445	1344
GTC GTG GCA ACA GAC GCT CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp 450 455 460	1392
TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser 465 470 475 480	1440
TTG GAT CCC ACC TTC ACC ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp Ala 485 490 495	1488
G TG TCG CGC TCG CAG CGG CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly 500 505 510	1536
ATC TAC AGG TTT GTG ACT CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe Asp 515 520 525	1584
TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG	1632

Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu			
530	535	540	
CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA			1680
Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr			
545	550	555	560
CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC			1728
Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val			
565	570	575	
TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG			1776
Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys			
580	585	590	
CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG			1824
Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val			
595	600	605	
TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG			1872
Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys			
610	615	620	
TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG			1920
Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu			
625	630	635	640
TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA			1968
Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile			
645	650	655	
ACC AAA TAC ATC ATG GCA TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT			2016
Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val Thr			
660	665	670	

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2016 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG

48

168

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro			
1	5	10	15
CGC GGC AGC CAT ATG GCT TAC TCT CTG ACT ACG GGT TCT GTT GTT ATT			96
Arg Gly Ser His Met Ala Tyr Ser Leu Thr Thr Gly Ser Val Val Ile			
20	25	30	
GTT GGT AGA ATT ATT TTA TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC			144
Val Gly Arg Ile Ile Leu Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser			
35	40	45	
CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC			192
Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly			
50	55	60	
CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA			240
Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala			
65	70	75	80
ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT			288
Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val			
85	90	95	
TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC			336
Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile			
100	105	110	
ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG			384
Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala			
115	120	125	
CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC			432
Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp			
130	135	140	
CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG			480
Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg			
145	150	155	160
GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG			528
Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu			
165	170	175	
AAG GGC TCT GCT GGT GGT CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG			576
Lys Gly Ser Ala Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala Val			
180	185	190	
GGC ATC TTC CGG GCT GCC GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG			624
Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val			
195	200	205	
GAC TTT GTG CCC GTA GAG TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC			672
Asp Phe Val Pro Val Glu Ser Met Glu Thr Thr Met Arg Ser Pro Val			
210	215	220	
TTC ACG GAC AAC TCA TCC CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG			720
Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Pro Gln Ser Phe Gln Val			
225	230	235	240

GCC CAC CTA CAC GCT CCC ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro 245 250 255	768
GCT GCA TAT GCA GCC CAA GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser 260 265 270	816
GTT GCC GCT ACC TTA GGG TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly 275 280 285	864
ATT GAC CCC AAC ATC AGA ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ala 290 295 300	912
CCC GTC ACA TAC TCT ACC TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys 305 310 315 320	960
TCT GGG GGC GCT TAT GAC ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr 325 330 335	1008
GAC TCG ACT ACA ATC TTG GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu 340 345 350	1056
ACG GCT GGA GCG CGG CTT GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly 355 360 365	1104
TCG GTC ACC GTG CCA CAC CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Asn 370 375 380	1152
ACT GGA GAG ATC CCC TTC TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile 385 390 395 400	1200
AGG GGG GGA AGG CAT CTC ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC Arg Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp 405 410 415	1248
GAG CTC GCC GCA AAG CTG TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr 420 425 430	1296
TAC CGG GGG CTC GAT GTG TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val 435 440 445	1344
GTC GTG GCA ACA GAC GCT CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp 450 455 460	1392
TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC	1440

170

Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser				1488
465 470 475 480				
TTG GAT CCC ACC TTC ACC ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA				
Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Val Pro Gln Asp Ala				
485 490 495				
GTG TCG CGC TCG CAG CGG CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC				1536
Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly				
500 505 510				
ATC TAC AGG TTT GTG ACT CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT				1584
Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe Asp				
515 520 525				
TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG				1632
Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu				
530 535 540				
CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA				1680
Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr				
545 550 555 560				
CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC				1728
Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val				
565 570 575				
TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG				1776
Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys				
580 585 590				
CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG				1824
Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val				
595 600 605				
TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG				1872
Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys				
610 615 620				
TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG				1920
Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu				
625 630 635 640				
TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA				1968
Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile				
645 650 655				
ACC AAA TAC ATC ATG GCA TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT				2016
Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val Thr				
660 665 670				

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

71

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT CCT GCT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT	144
Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu	
35 40 45	
GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG	192
Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu	
50 55 60	
GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC	240
Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr	
65 70 75 80	
TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG	288
Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys	
85 90 95	
ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG	336
Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val	
100 105 110	
GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG	384
Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu	
115 120 125	
ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT	432
Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His	
130 135 140	
GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG	480
Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu	
145 150 155 160	
CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA	528
Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro	
165 170 175	

CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val 180 185 190	576
TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser 195 200 205	624
ATG GAA ACT ACT ATG CGG TCT TGA Met Glu Thr Thr Met Arg Ser 210 215	648

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro 1 5 10 15	48
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30	96
TCT CCT GCT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu 35 40 45	144
GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu 50 55 60	192
GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr 65 70 75 80	240
TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys 85 90 95	288
ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG	336

Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val			
100	105	110	
GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG		384	
Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu			
115	120	125	
ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT		432	
Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His			
130	135	140	
GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG		480	
Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu			
145	150	155	160
CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA		528	
Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro			
165	170	175	
CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA		576	
Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val			
180	185	190	
TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC		624	
Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser			
195	200	205	
ATG GAA ACT ACT ATG CGG TCT TGA		648	
Met Glu Thr Thr Met Arg Ser			
210	215		

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
- (B) LOCATION: 1..648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG		48	
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro			
1	5	10	15
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA		96	
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu			
20	25	30	

174

TCT GGT GGT TCT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT .	144
Ser Gly Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu	
35 40 45	
GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG	192
Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu	
50 55 60	
GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC	240
Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr	
65 70 75 80	
TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG	288
Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys	
85 90 95	
ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG	336
Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val	
100 105 110	
GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG	384
Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu	
115 120 125	
ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT	432
Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His	
130 135 140	
GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG	480
Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu	
145 150 155 160	
CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA	528
Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro	
165 170 175	
CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA	576
Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val	
180 185 190	
TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC	624
Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser	
195 200 205	
ATG GAA ACT ACT ATG CGG TCT TGA	648
Met Glu Thr Thr Met Arg Ser	
210 215	

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

125

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	48
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT ATT GTT GGT AGA ATT ATT TTA Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	96
20 25 30	
TCT GGT TCT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT Ser Gly Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu	144
35 40 45	
GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu	192
50 55 60	
GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr	240
65 70 75 80	
TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys	288
85 90 95	
ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val	336
100 105 110	
GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu	384
115 120 125	
ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His	432
130 135 140	
GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu	480
145 150 155 160	
CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro	528
165 170 175	
CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val	576
180 185 190	
TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC	624

Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser
195							200						205		

ATG	GAA	ACT	ACT	ATG	CGG	TCT	TGA								648
Met	Glu	Thr	Thr	Met	Arg	Ser									
210						215									

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1941 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ATG	CAT	ATG	CAT	CAT	CAT	CAC	CAT	CAT	CTG	GTG	CCG	CGC	GGC	AGC	GCG	48
Met	His	Met	His	His	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala	
1		5							10					15		

CCC	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	CTA	CTT	GGT	TGC	AAG	96
Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Lys	
20		25							30							

ATC	ACT	AGC	CTT	ACA	GGC	CGG	GAC	AAG	AAC	CAG	GTC	GAG	GGA	GAG	GTT	144
Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val	
35		40							45							

CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	ACC	TGC	GTC	AAC	192
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	
50		55							60							

GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	AAG	ACC	TTA	GCC	240
Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	
65		70						75				80				

GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	GTG	GAC	CAG	GAC	288
Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	
85		90							95							

CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	TTG	ACA	CCA	TGC	336
Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	
100		105							110							

ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	CAT	GCT	GAC	GTC	384
Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	
115		120							125							

ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro 130 135 140	432
AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT CCA CTG CTC TGC Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys 145 150 155 160	480
CCT TCG GGG CAC GCT GTG GGC ATC TTC CCG GCT GCC GTA TGC ACC CGG Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg 165 170 175	528
GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC ATG GAA ACT Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr 180 185 190	576
ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC CCC CCG GCC GTA Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val 195 200 205	624
CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC ACT GGC AGC GGC Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly 210 215 220	672
AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA GGG TAC AAG GTG Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val 225 230 235 240	720
CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG TTT GGG GCG TAT Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr 245 250 255	768
ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA ACT GGG GTA AGG Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg 260 265 270	816
ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC TAT GGC AAG TTT Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe 275 280 285	864
CTT GCC GAT GGT TGC TCT GGG GGC GCT TAT GAC ATC ATA ATA TGT Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys 290 295 300	912
GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG GGC ATC GGC ACA Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr 305 310 315 320	960
GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT GTC GTG CTC GCC Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala 325 330 335	1008
ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC CCA AAC ATC GAG Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu 340 345 350	1056
GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC TAT GGC AAA GCC Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala	1104

355	360	365	
ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC ATT TTC TGT CAT Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His 370 375 380			1152
TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG TCA GGC CTC GGA Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly 385 390 395 400			1200
ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG TCC GTC ATA CCA Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro 405 410 415			1248
ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT CTG ATG ACG GGC Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met Thr Gly 420 425 430			1296
TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr 435 440 445			1344
CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC ATT GAG ACG ACG Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr 450 455 460			1392
ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG CGG GGT AGG ACT Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr 465 470 475 480			1440
GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT CCG GGA GAA CGG Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg 485 490 495			1488
CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala 500 505 510			1536
GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu 515 520 525			1584
CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 530 535 540			1632
GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 545 550 555 560			1680
TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val 565 570 575			1728
GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser 580 585 590			1776

TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His 595 600 605	1824
GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val 610 615 620	1872
ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 625 630 635 640	1920
GAC CTG GAG GTC GTT ACG TAG Asp Leu Glu Val Val Thr 645	1941

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1941 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ATG CAT ATG CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG Met His Met His His His His His His Leu Val Pro Arg Gly Ser Ala 1 5 10 15	48
CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile 20 25 30	96
AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val 35 40 45	144
CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn 50 55 60	192
GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala 65 70 75 80	240
GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC	288

180

Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp			
85	90	95	
CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC			336
Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys			
100	105	110	
ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC			384
Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val			
115	120	125	
ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC			432
Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro			
130	135	140	
AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA CTG CTC TGC			480
Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys			
145	150	155	160
CCT TCG GGG CAC GCT GTG GGC ATC TTC CCG GCT GCC GTA TGC ACC CGG			528
Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg			
165	170	175	
GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC ATG GAA ACT			576
Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr			
180	185	190	
ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC CCC CCG GCC GTA			624
Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val			
195	200	205	
CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC ACT GGC AGC GGC			672
Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly			
210	215	220	
AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA GGG TAC AAG GTG			720
Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val			
225	230	235	240
CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG TTT GGG GCG TAT			768
Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr			
245	250	255	
ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA ACT GGG GTA AGG			816
Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg			
260	265	270	
ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC TAT GGC AAG TTT			864
Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe			
275	280	285	
CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC ATC ATA ATA TGT			912
Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys			
290	295	300	
GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG GGC ATC GGC ACA			960
Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr			
305	310	315	320

GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT GTC GTG CTC GCC Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala 325 330 335	1008
ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC CCA AAC ATC GAG Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu 340 345 350	1056
GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC TAT GGC AAA GCC Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala 355 360 365	1104
ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC ATT TTC TGT CAT Ile Pro Ile Glu Ala Ile Arg Gly Arg His Leu Ile Phe Cys His 370 375 380	1152
TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG TCA GGC CTC GGA Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly 385 390 395 400	1200
ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG TCC GTC ATA CCA Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro 405 410 415	1248
ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT CTG ATG ACG GGC Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met Thr Gly 420 425 430	1296
TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr 435 440 445	1344
CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC ATT GAG ACG ACG Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr 450 455 460	1392
ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG CGG GGT AGG ACT Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr 465 470 475 480	1440
GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT CCG GGA GAA CGG Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg 485 490 495	1488
CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala 500 505 510	1536
GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu 515 520 525	1584
CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 530 535 540	1632
GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC	1680

182

Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His			
545	550	555	560
TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA			1728
Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val			
565	570	575	
GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCT CCA TCA			1776
Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser			
580	585	590	
TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC			1824
Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His			
595	600	605	
GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC			1872
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val			
610	615	620	
ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC			1920
Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala			
625	630	635	640
GAC CTG GAG GTC GTT ACG TAG			1941
Asp Leu Glu Val Val Thr			
645			

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ATG CAT ATG CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG			48
Met His Met His His His His His Leu Val Pro Arg Gly Ser Ala			
1	5	10	15
CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC			96
Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile			
20	25	30	
ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT			144
Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val			
35	40	45	

183

CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn 50 55 60	192
GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala 65 70 75 80	240
GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp 85 90 95	288
CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys 100 105 110	336
ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val 115 120 125	384
ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro 130 135 140	432
AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT CCA CTG CTC TGC Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Pro Leu Leu Cys 145 150 155 160	480
CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA TGC ACC CGG Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg 165 170 175	528
GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC ATG GAA ACT Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr 180 185 190	576
ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC CCC CCG GCC GTA Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val 195 200 205	624
CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC ACT GGC AGC GGC Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly 210 215 220	672
AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA GGG TAC AAG GTG Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val 225 230 235 240	720
CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG TTT GGG GCG TAT Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr 245 250 255	768
ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA ACT GGG GTA AGG Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg 260 265 270	816
ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC TAT GGC AAG TTT	864

Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe			
275	280	285	
CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC ATC ATC ATA ATA TGT			912
Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys			
290	295	300	
GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG GGC ATC GGC ACA			960
Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr			
305	310	315	320
GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT GTC GTG CTC GCC			1008
Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala			
325	330	335	
ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC CCA AAC ATC GAG			1056
Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu			
340	345	350	
GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC TAT GGC AAA GCC			1104
Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala			
355	360	365	
ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC ATT TTC TGT CAT			1152
Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His			
370	375	380	
TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG TCA GGC CTC GGA			1200
Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly			
385	390	395	400
ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG TCC GTC ATA CCA			1248
Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro			
405	410	415	
ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT CTG ATG ACG GGC			1296
Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met Thr Gly			
420	425	430	
TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC			1344
Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr			
435	440	445	
CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC ATT GAG ACG ACG			1392
Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr			
450	455	460	
ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG CGG GGT AGG ACT			1440
Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr			
465	470	475	480
GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT CCG GGA GAA CGG			1488
Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg			
485	490	495	
CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG			1536
Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala			
500	505	510	

GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu 515 520 525	1584
CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 530 535 540	1632
GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 545 550 555 560	1680
TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val 565 570 575	1728
GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser 580 585 590	1776
TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His 595 600 605	1824
GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val 610 615 620	1872
ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 625 630 635 640	1920
GAC CTG GAG GTC GTT ACG TAG Asp Leu Glu Val Val Thr 645	1941

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ATG CAT ATG CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG

48

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	Met	His	Met	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala	
1								10					15		
CCC	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	CTA	CTT	GGT	TGC	ATC
Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile
								20					30		
ATC	ACT	AGC	CTT	ACA	GGC	CGG	GAC	AAG	AAC	CAG	GTC	GAG	GGA	GAG	GTT
Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val
								35					45		
CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	ACC	TGC	GTC	AAC
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn
								50					60		
GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	AAG	ACC	TTA	GCC
Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala
								65					80		
GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	GTG	GAC	CAG	GAC
Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp
								85					95		
CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	TTG	ACA	CCA	TGC
Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys
								100					110		
ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	CAT	GCT	GAC	GTC
Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val
								115					125		
ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	CTG	CTC	TCC	CCC
Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro
								130					140		
AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	CCA	CTG	CTC	TGC	
Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys
								145					155		160
CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	GTA	TGC	ACC	CGG
Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg
								165					175		
GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	TCC	ATG	GAA	ACT
Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr
								180					190		
ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	CCC	CCG	GCC	GTA
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val
								195					205		
CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	ACT	GGC	AGC	GGC
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly
								210					220		
AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	GGG	TAC	AAG	GTG
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val
								225					235		240

CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG TTT GGG GCG TAT Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr 245 250 255	768
ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA ACT GGG GTA AGG Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg 260 265 270	816
ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC TAT GGC AAG TTT Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe 275 280 285	864
CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC ATC ATA ATA TGT Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys 290 295 300	912
GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG GGC ATC GGC ACA Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr 305 310 315 320	960
GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT GTC GTG CTC GCC Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala 325 330 335	1008
ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC CCA AAC ATC GAG Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu 340 345 350	1056
GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC TAT GGC AAA GCC Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala 355 360 365	1104
ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC ATT TTC TGT CAT Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His 370 375 380	1152
TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG TCA GGC CTC GGA Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly 385 390 395 400	1200
ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG TCC GTC ATA CCA Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro 405 410 415	1248
ACT TCC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT CTG ATG ACG GGC Thr Ser Gly Asp Val Val Val Ala Thr Asp Ala Leu Met Thr Gly 420 425 430	1296
TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr 435 440 445	1344
CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC ATT GAG ACG ACG Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr 450 455 460	1392
ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG CGG GGT AGG ACT	1440

Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr					
465	470	475	480		
Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg					
485	490	495			1488
CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG					
Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala					
500	505	510			1536
Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu					
515	520	525			1584
CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG					
Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu					
530	535	540			1632
GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC					
Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His					
545	550	555	560		1680
TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA					
Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val					
565	570	575			1728
GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA					
Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser					
580	585	590			1776
TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC					
Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His					
595	600	605			1824
GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC					
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val					
610	615	620			1872
ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC					
Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala					
625	630	635	640		1920
GAC CTG GAG GTC GTT ACG TAG					
Asp Leu Glu Val Val Thr					
645					1941

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1941 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

189

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..1941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATG CAT ATG CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG	48
Met His Met His His His His His Leu Val Pro Arg Gly Ser Ala	
1 5 10 15	
CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC	96
Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile	
20 25 30	
ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT	144
Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val	
35 40 45	
CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC	192
Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn	
50 55 60	
GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC	240
Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala	
65 70 75 80	
GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC	288
Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp	
85 90 95	
CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC	336
Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys	
100 105 110	
ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC	384
Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val	
115 120 125	
ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC	432
Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro	
130 135 140	
AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT CCA CTG CTC TGC	480
Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys	
145 150 155 160	
CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA TGC ACC CGG	528
Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg	
165 170 175	
GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC ATG GAA ACT	576
Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr	
180 185 190	

190

ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC CCC CCG GCC GTA Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val 195 200 205	624
CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC ACT GGC AGC GGC Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly 210 215 220	672
AAG AGT ACT AAA GTG CCG GCT GCC TAC GCA GCC CAA GGG TAC AAG GTG Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val 225 230 235 240	720
CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG TTT GGG GCG TAT Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr 245 250 255	768
ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA ACT GGG GTA AGG Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg 260 265 270	816
ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC TAT GGC AAG TTT Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe 275 280 285	864
CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC ATC ATA ATA TGT Leu Ala Asp Gly Gly Cys Ser Gly Ala Tyr Asp Ile Ile Ile Cys 290 295 300	912
GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG GGC ATC GGC ACA Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr 305 310 315 320	960
GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT GTC GTG CTC GCC Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala 325 330 335	1008
ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC CCA AAC ATC GAG Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu 340 345 350	1056
GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC TAT GGC AAA GCC Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala 355 360 365	1104
ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC ATT TTC TGT CAT Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His 370 375 380	1152
TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG TCA GGC CTC GGA Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly 385 390 395 400	1200
ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG TCC GTC ATA CCA Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro 405 410 415	1248
ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT CTG ATG ACG GGC Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met Thr Gly	1296

	420	425	430	
TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr	435	440	445	1344
CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC ATT GAG ACG ACG Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr	450	455	460	1392
ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG CGG GGT AGG ACT Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr	465	470	475	1440
GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT CCG GGA GAA CGG Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg	485	490	495	1488
CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala	500	505	510	1536
GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu	515	520	525	1584
CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu	530	535	540	1632
GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His	545	550	555	1680
TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val	565	570	575	1728
GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser	580	585	590	1776
TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His	595	600	605	1824
GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val	610	615	620	1872
ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala	625	630	635	1920
GAC CTG GAG GTC GTT ACG TAG Asp Leu Glu Val Val Thr	645			1941

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(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCUCGCCCGG GGAUCCUCUA GGAAUACACG UUCGAU 36

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CUAGAGGAUC CCCGGGCGAG CCCUAUAGUG AGUCGU 36

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GCTCGCCCGG GGATCCTCTA G 21

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cont
